

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: July 7, 2004, 17:46:47 ; Search time 1892.13 Seconds
(without alignments)
1600.756 Million cell updates/sec

Title: US-10-018-786-7

Perfect score: 702
Sequence: 1 aatggctttgtttagtc.....cggtgccgatgttttgtga 702

Scoring table: IDENTITY_NUC
GapOp 10.0 , GapExt 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmpl:*

1: gb_ba:*

2: gb_btgc:*

3: gb_in:*

4: gb_mam:*

5: gb_ny:*

6: gb_pat:*

7: gb_ph:*

8: gb_sj:*

9: gb_pr:*

10: gb_ror:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vii:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_ln:*

19: em_mui:*

20: em_cm:*

21: em_cr:*

22: em_lov:*

23: em_dat:*

24: em_ph:*

25: em_pl:*

26: em_rc:*

27: em_sts:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	702	100.0	702	6	AX01806		AX01806 Sequence
2	702	100.0	11629	1	AE01222	Xanthomonas	AE01222 Xanthomonas
3	479	6	68.3	1629	XC033548		U33548 Xanthomonas
4	474	8	67.6	13551	AE011666		AE011666 Xanthomonas
5	473	2	67.4	29206	AF49777	Xanthomonas	AF49777 Xanthomonas
c	6	460	4	65.6	8230	1	AY139029
c	7	460	4	65.6	10996	1	AF026197
c	8	460	4	65.6	19304	1	AB05311
c	9	460	4	65.6	23614	1	AY205561
c	10	460	4	65.6	100258	1	AY055110
c	11	116	8	20.9	197030	1	AL646081
c	12	137	2	19.5	23407	1	AJ245811
c	13	101	4	14.4	29814	1	AF074878
c	14	74	10.5	113193	1	AF357202	Streptomyces
c	15	74	10.5	113193	6	AK703543	Sequence
c	16	69	6	9.9	138390	14	AY261359
c	17	69	6	9.9	290452	2	AC079167
c	18	69	4.8	313800	1	SC039114	Mus musculus
c	19	68	4.8	219952	2	AC064804	Streptomyces
c	20	67	2	9.6	6297	6	AK598629
c	21	67	2	9.6	50543	2	AK598617
c	22	66	6	9.3	181850	2	BX276102
c	23	66	4	9.5	309050	1	AK939117
c	24	66	4	9.4	158911	8	AC107619
c	25	65	8	9.4	5317	14	SH010303
c	26	65	4	9.3	82746	1	AF053501
c	27	65	4	9.3	134544	2	AC135396
c	28	63	9.3	5894	1	AY117133	Seicharop
c	29	65	9.3	11238	6	AX67991	Sequence
c	30	65	9.3	60196	6	AX67977	Sequence
c	31	64	6	9.2	1133	11	AI1684264
c	32	64	6	9.2	181850	2	BX276102
c	33	64	4	9.2	239130	2	AC079420

Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Moreira, L.M., Novo, M.T.M., Nenck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, N.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira, Jr., H.A., Rossi, A., Sena, J.A.D., Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.	TITLE	Comparison of the genomes of two <i>Xanthomonas</i> pathogens with differing host specificities
JOURNAL	Nature	417 (6887), 459-463 (2002)
PUBMED	12022145	
REFERENCE	2 (bases 1 to 11629)	
AUTHORS	da Silva, A.C.R., Ferro, J.A., Reinoeh, F.C., Farah, C.S., Furlan, L.R., Quaglio, R.B., Monteiro-Vitorelo, C.B., Van Sluys, M.A., Amieva Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarote, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, F., El-Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Giorgi, C.C., Gruber, A., Katsuyama, A.M., Kishii, I.T., Leite, Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Moreira, N.M., Nenck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira, Jr., H.A., Rossi, A., Sena, J.A.D., Souza, R.F., Spinola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.	
TITLE	Submitted (28-NOV-2001) Departamento de Bioquimica, Universidade de São Paulo, Av. Prof. Lineu Prestes 746, São Paulo, SP 05508-900, Brazil	
FEATURES	source	Location/Qualifiers
		1. 1.11629 /organism="Xanthomonas campestris pv. campestris str. ATCC 33913"
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 TSVPESKLTMVMSVEGLYENVSYTVEGGESDAQFASASPRAWWVPGALA
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 located using Blastx/Glimmer/Genemark"

Db 6818 ACCGGCCTGTTGAGAACCGATTCGGTGATCAGTGGCAAGTCCGGAGTCTCCGGCGTCATTCGC 6877
 Gy 661 CGGTTTGGCAAGCGGAGCGGATGGCTCCGGATGCTGGGA 702
 Db 6878 CGGTGTTGCCACGCCGCGGAGGGTGGCGAGTCGTTGCA 6919
 Search completed: July 7, 2004, 23:54:59
 Job time : 1837.13 secs

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OM nucleic - nucleic search, using sw model
 Run on: July 7, 2004, 17:42:57 ; Search time 205.168 Seconds
 (without alignments)
 1455.578 Million cell updates/sec

```

Title: US-10-018-786-7
Perfect score: 702
Sequence: 1 atcgcttttggctgaggc.....cgggtccggatcttgatcgaa 702

Scoring table: IDENTITY_NUC
GapOp 10.0 , GapExt 1.0

Searched: 3373863 seeds, 21409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
N_Geneseq_29Jan04:*
  1: geneseqn180s:*
  2: geneseqn1890s:*
  3: geneseqn200s:*
  4: geneseqn2001s:*
  5: geneseqn2001s:*
  6: geneseqn2002s:*
  7: geneseqn2003s:*
  8: geneseqn2003s:*
  9: geneseqn2003s:*
  10: geneseqn2004s:*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB	ID	Description
1	702	100.0	702	5	AB157895	Ab157895 Partial h
c 2	74	10.5	113193	7	AAD5465	Aad5465 Streptomy
3	67.2	9.6	6297	7	AAD54236	Aad54236 Streptomy
4	67.2	9.6	50543	7	AAD54230	Aad54230 Streptomy
5	67	9.5	114955	2	AAK53491	Aak53491 Human ade
c 6	65.4	9.3	2247	7	AAL61177	Aal61177 Actinosyn
7	65.4	9.3	82746	7	AAL61224	Aal61224 Actinosyn

Db GenCore version 5.1.6
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 Qy OM nucleic - nucleic search, using sw model
 Do Run on: July 7, 2004, 20:18:17 ; Search time 1351.57 Seconds
 (without alignments)
 15510.269 Million cell updates/sec

Title: US-10-018-786-7
 Perfect score: 702
 Sequence: 1 atgcgtcttggctgaggct.....cggtccggatgttttgtga 702

Scoring table: IDENTITY_NJC
 GapOp 10.0 , GapExt 1.0

Searched: 27513289 seqs., 14931090276 residues
 Total number of hits satisfying chosen parameters: 5506578

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : EST:*

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  1: em_estba:*
  2: em_esthum:*
  3: em_estin:*
  4: em_estmu:*
  5: em_estov:*
  6: em_estpl:*
  7: em_estro:*
  8: em_htc:*
  9: gb_est1:*
  10: gb_est2:*
  11: gb_htc:*
  12: gb_est3:*
  13: gb_est4:*
  14: gb_est5:*
  15: em_estfun:*
  16: em_estcom:*
  17: em_gss_hum:*
  18: em_gss_inv:*
  19: em_gss_pn:*
  20: em_gss_vrt:*
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  26: em_gss_dig:*
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Search completed: July 7, 2004, 21:07:53
 Job time : 209.168 secs

28: gb_gss1:
29: gb_gss2:

Search completed: July 8, 2004, 01:54:11
Job time : 1354.57 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	83.4	11.9	935	CNS006XK	AL066051 Drosophil
c 2	83	11.8	1131	29	AG042920 Pan trogl
c 3	81.6	11.6	1244	12	BG846745 1024014H0
c 4	77.4	11.0	1201	13	BX340009 BX415111
c 5	76.8	10.9	982	13	BX415111 BX415111
c 6	76.4	10.9	925	29	AL053013 Drosophil
c 7	75.4	10.7	1452	29	AG032879 Pan trogl
c 8	74.2	10.6	925	29	CHS091P AL053013 Drosophil
c 9	73	10.4	1043	29	AS128304 Pan trogl
c 10	72.6	10.3	1134	29	AG043044 Pan trogl
c 11	72	10.3	893	28	AS1193531 SP1003-B
c 12	71.8	10.2	1998	29	AG030579 Pan trogl
c 13	71.2	10.1	1101	29	AG039443 Pan trogl
c 14	71.2	10.1	1201	13	BX340009 BX340009
c 15	71	10.1	1104	29	AG062490 Pan trogl
c 16	70.8	10.1	932	29	CHS0012Q AL066742 Drosophil
c 17	70.8	10.1	1610	28	B2569386 Pacs2-164
c 18	70.6	10.1	1189	29	AG030608 Pan trogl
c 19	70.4	10.0	1421	28	B2569488 Pacs2-164
c 20	70.2	10.0	1798	29	AG171124 Pan trogl
c 21	70	10.0	935	29	CHS006XK AL066651 Drosophil
c 22	70	10.0	1438	28	B2557331 Pacs1-60
c 23	70	10.0	1538	29	AG030607 Pan trogl
c 24	69.4	9.9	1452	29	AG032979 Pan trogl
c 25	69.4	9.9	1626	10	AN731212 GA_Ea001
c 26	69.2	9.9	896	29	AG159205 Pan trogl
c 27	69.2	9.9	1026	28	B2569417 Pacs2-164
c 28	69.2	9.9	1289	29	AG039481 Pan trogl
c 29	69.2	9.9	1348	29	CG752544 P047-2-C1
c 30	68.8	9.8	1157	12	BM466479 AGENCOURT
c 31	68.6	9.8	932	29	AL066742 Drosophil
c 32	68.6	9.8	1132	14	CR210297 FG502209
c 33	68.4	9.7	1057	29	AL276477 Tetraodon
c 34	68.4	9.7	1083	14	CK206171 FG501775
c 35	68.2	9.7	1165	29	AG030649 Pan trogl
c 36	68.2	9.7	1201	13	BX405071 BX405071
c 37	67.6	9.6	1387	10	AW731151 GA_Ea001
c 38	67.4	9.6	1542	29	AG032943 Pan trogl
c 39	67.2	9.6	1200	13	BX415896 BX415896
c 40	67	9.5	1120	29	AG136785 Pan trogl
c 41	66.6	9.5	842	29	AG058791 Pan trogl
c 42	66.4	9.5	1124	29	AG041123 Pan trogl
c 43	66.4	9.5	1232	29	AG072425 Pan trogl
c 44	66.4	9.5	1273	12	BMS62039 AGECOUNT
c 45	66.4	9.5	1277	29	AG060256 Pan trogl